Untitled

```
RESULT 22
AAU97785
I D
       AAU97785 standard; peptide; 4 AA.
XX
AC
       AAU97785;
XX
DT
       07-OCT-2002 (first entry)
XX
DE
       Tumour specific peptide sequence #1.
XX
      Tumour i maging; radiodiagnosis; tumour; cancer; breast; ovary; prostate; endometrium, bladder; lung; oesophagus; colon; pancreas; brain; liver metastasis; neuroendocrine tumour; carcinoid.
KW
KW
KW
XX
XXX
FIT
       Unidentified.
       Key
                              Location/Qualifiers
FT
       Modified-site
FT
                              /label = OTHER
FT
                              /note= "OTHER= Optionally labelled with technetium-99m"
FT
       M sc-difference 2
FT
                              / not e= "D-form residue"
FT
       Modified-site
/label = OTHER
                             /note= "OTHER= Optionally linked with 4-aminobutyric
                              aci d"
       US6395255-B1.
       28- MAY- 2002.
       15-JUN-1999;
                            99US-00333842.
                            98US-0089364P.
       15-JUN-1998;
       (UYJE-) UNIV JEFFERSON THOMAS.
       Thakur ML;
       WPI: 2002-556090/59.
       Compositions, useful as radiodiagnostic agent for imaging tumors,
       comprises tumor specific sequence linked to radionuclide moiety.
       Claim 7; Col 17; 17pp; English.
       The invention relates to a composition comprising a tumour specific
      sequence linked to a radionuclide moiety. A reagent for radiolabelling a tumour imaging agent comprises four amino acids, which covalently link the radionuclide to the amino group, complexed with a tumour specific sequence and enables the reagent to bind to a tumour. The composition is useful as a radiodiagnostic agent for imaging tumours (such as breast,
       ovarian, endometrial, prostate, bladder, lung, oesophageal, colonic and pancreatic cancers and neuroendocrine and brain tumors), liver
       metastases, and carcinoids in mammals. This sequence represents a
       radionuclide moiety used in the scope of the invention
       Sequence 4 AA;
                                                Score 16; DB 5;
Pred. No. 2.9e+06;
   Query Match
                                     100.0%
                                                                         Length 4;
   Best Local Similarity
                                     100.0%
                                              0; M smatches
   Mat ches
                  3; Conservative
                                                                             Indels
                                                                                                  Gaps
                                                                                                             0:
```

Qy	1 AGG 3	
Db	 2 AGG 4	